

#15

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/327,563B

DATE: 04/16/2001  
TIME: 15:53:09

Input Set : A:\Seqlist.txt  
Output Set: N:\CRF3\04162001\I327563B.raw

ENTERED

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4 <110> APPLICANT: Svendsen, Allan
5   Bisgard-Frantzen, Henrik
6   Borchert, Torben Vedel
8 <120> TITLE OF INVENTION: Alpha-Amylase Mutants
11 <130> FILE REFERENCE: 0776/1F216-US2
13 <140> CURRENT APPLICATION NUMBER: 09/327,563B
14 <141> CURRENT FILING DATE: 1999-06-08
16 <150> PRIOR APPLICATION NUMBER: 08/683,838
17 <151> PRIOR FILING DATE: 1996-07-18
19 <160> NUMBER OF SEQ ID NOS: 16
21 <170> SOFTWARE: FastSEQ for Windows Version 3.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1920
25 <212> TYPE: DNA
26 <213> ORGANISM: B. licheniformis
28 <220> FEATURE:
29 <221> NAME/KEY: sig_peptide
30 <222> LOCATION: (334)...(420)
32 <221> NAME/KEY: mat_peptide
33 <222> LOCATION: (421)...(1869)
35 <221> NAME/KEY: CDS
36 <222> LOCATION: (334)...(1869)
38 <400> SEQUENCE: 1
39   cggaagattg gaagtacaaa aataagcaaa agattgtcaa tcatgtcatg agccatgcgg      60
40   gagacggaaa aatcgtctta atgcacgata tttatgcaac gttcgcagat gctgctgaag      120
41   agattattaa aaagctgaaa gcaaaaaggct atcaattggg aactgtatct cagcttgaag      180
42   aagtgaagaa gcagagaggc tattgaataa atgagtagaa gcgcatatc ggcgcttttc      240
43   ttttgaaga aaatataggg aaaatggtag ttgttaaaaa ttcggaatat ttatacaaca      300
44   tcatatgttt cacattgaaa ggggaggaga atc atg aaa caa caa aaa cgg ctt      354
45                                     Met Lys Gln Gln Lys Arg Leu
46                                     -25
48   tac gcc cga ttg ctg acg ctg tta ttt gcg ctc atc ttc ttg ctg cct      402
49   Tyr Ala Arg Leu Leu Thr Leu Leu Phe Ala Leu Ile Phe Leu Leu Pro
50   -20                               -15                               -10
52   cat tct gca gca gcg gcg gca aat ctt aat ggg acg ctg atg cag tat      450
53   His Ser Ala Ala Ala Ala Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr
54   -5                               1                               5                               10
56   ttt gaa tgg tac atg ccc aat gac ggc caa cat tgg agg cgt ttg caa      498
57   Phe Glu Trp Tyr Met Pro Asn Asp Gly Gln His Trp Arg Arg Leu Gln
58   15                               20                               25
60   aac gac tcg gca tat ttg gct gaa cac ggt att act gcc gtc tgg att      546
61   Asn Asp Ser Ala Tyr Leu Ala Glu His Gly Ile Thr Ala Val Trp Ile
62   30                               35                               40
64   ccc ccg gca tat aag gga acg agc caa gcg gat gtg ggc tac ggt gct      594
65   Pro Pro Ala Tyr Lys Gly Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala
66   45                               50                               55
68   tac gac ctt tat gat tta ggg gag ttt cat caa aaa ggg acg gtt cgg      642

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69 Tyr Asp Leu Tyr Asp Leu Gly Glu Phe His Gln Lys Gly Thr Val Arg
70      60      65      70
72 aca aag tac ggc aca aaa gga gag ctg caa tct gcg atc aaa agt ctt      690
73 Thr Lys Tyr Gly Thr Lys Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu
74      75      80      85      90
76 cat tcc cgc gac att aac gtt tac ggg gat gtg gtc atc aac cac aaa      738
77 His Ser Arg Asp Ile Asn Val Tyr Gly Asp Val Val Ile Asn His Lys
78      95      100      105
80 ggc ggc gct gat gcg acc gaa gat gta acc gcg gtt gaa gtc gat ccc      786
81 Gly Gly Ala Asp Ala Thr Glu Asp Val Thr Ala Val Glu Val Asp Pro
82      110      115      120
84 gct gac cgc aac cgc gta att tca gga gaa cac cta att aaa gcc tgg      834
85 Ala Asp Arg Asn Arg Val Ile Ser Gly Glu His Leu Ile Lys Ala Trp
86      125      130      135
88 aca cat ttt cat ttt ccg ggg cgc ggc agc aca tac agc gat ttt aaa      882
89 Thr His Phe His Phe Pro Gly Arg Gly Ser Thr Tyr Ser Asp Phe Lys
90      140      145      150
92 tgg cat tgg tac cat ttt gac gga acc gat tgg gac gag tcc cga aag      930
93 Trp His Trp Tyr His Phe Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys
94      155      160      165      170
96 ctg aac cgc atc tat aag ttt caa gga aag gct tgg gat tgg gaa gtt      978
97 Leu Asn Arg Ile Tyr Lys Phe Gln Gly Lys Ala Trp Asp Trp Glu Val
98      175      180      185
100 tcc aat gaa aac ggc aac tat gat tat ttg atg tat gcc gac atc gat      1026
101 Ser Asn Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp
102      190      195      200
104 tat gac cat cct gat gtc gca gca gaa att aag aga tgg ggc act tgg      1074
105 Tyr Asp His Pro Asp Val Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp
106      205      210      215
108 tat gcc aat gaa ctg caa ttg gac ggt ttc cgt ctt gat gct gtc aaa      1122
109 Tyr Ala Asn Glu Leu Gln Leu Asp Gly Phe Arg Leu Asp Ala Val Lys
110      220      225      230
112 cac att aaa ttt tct ttt ttg cgg gat tgg gtt aat cat gtc agg gaa      1170
113 His Ile Lys Phe Ser Phe Leu Arg Asp Trp Val Asn His Val Arg Glu
114      235      240      245      250
116 aaa acg ggg aag gaa atg ttt acg gta gct gaa tat tgg cag aat gac      1218
117 Lys Thr Gly Lys Glu Met Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp
118      255      260      265
120 ttg ggc gcg ctg gaa aac tat ttg aac aaa aca aat ttt aat cat tca      1266
121 Leu Gly Ala Leu Glu Asn Tyr Leu Asn Lys Thr Asn Phe Asn His Ser
122      270      275      280
124 gtg ttt gac gtg ccg ctt cat tat cag ttc cat gct gca tcg aca cag      1314
125 Val Phe Asp Val Pro Leu His Tyr Gln Phe His Ala Ala Ser Thr Gln
126      285      290      295
128 gga ggc ggc tat gat atg agg aaa ttg ctg aac ggt acg gtc gtt tcc      1362
129 Gly Gly Gly Tyr Asp Met Arg Lys Leu Leu Asn Gly Thr Val Val Ser
130      300      305      310
132 aag cat ccg ttg aaa tcg gtt aca ttt gtc gat aac cat gat aca cag      1410
133 Lys His Pro Leu Lys Ser Val Thr Phe Val Asp Asn His Asp Thr Gln

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134 315          320          325          330
136 ccg ggg caa tcg ctt gag tcg act gtc caa aca tgg ttt aag ccg ctt 1458
137 Pro Gly Gln Ser Leu Glu Ser Thr Val Gln Thr Trp Phe Lys Pro Leu
138          335          340          345
140 gct tac gct ttt att ctc aca agg gaa tct gga tac cct cag gtt ttc 1506
141 Ala Tyr Ala Phe Ile Leu Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe
142          350          355          360
144 tac ggg gat atg tac ggg acg aaa gga gac tcc cag cgc gaa att cct 1554
145 Tyr Gly Asp Met Tyr Gly Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro
146          365          370          375
148 gcc ttg aaa cac aaa att gaa ccg atc tta aaa gcg aga aaa cag tat 1602
149 Ala Leu Lys His Lys Ile Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr
150          380          385          390
152 gcg tac gga gca cag cat gat tat ttc gac cac cat gac att gtc ggc 1650
153 Ala Tyr Gly Ala Gln His Asp Tyr Phe Asp His His Asp Ile Val Gly
154          395          400          405          410
156 tgg aca agg gaa ggc gac agc tcg gtt gca aat tca ggt ttg gcg gca 1698
157 Trp Thr Arg Glu Gly Asp Ser Ser Val Ala Asn Ser Gly Leu Ala Ala
158          415          420          425
160 tta ata aca gac gga ccc ggt ggg gca aag cga atg tat gtc ggc cgg 1746
161 Leu Ile Thr Asp Gly Pro Gly Gly Ala Lys Arg Met Tyr Val Gly Arg
162          430          435          440
164 caa aac gcc ggt gag aca tgg cat gac att acc gga aac cgt tcg gag 1794
165 Gln Asn Ala Gly Glu Thr Trp His Asp Ile Thr Gly Asn Arg Ser Glu
166          445          450          455
168 ccg gtt gtc atc aat tcg gaa ggc tgg gga gag ttt cac gta aac ggc 1842
169 Pro Val Val Ile Asn Ser Glu Gly Trp Gly Glu Phe His Val Asn Gly
170          460          465          470
172 ggg tcg gtt tca att tat gtt caa aga tagaagagca gagaggacgg 1889
173 Gly Ser Val Ser Ile Tyr Val Gln Arg
174          475          480
176 atttctgaa ggaaatccgt ttttttattt t 1920
178 <210> SEQ ID NO: 2
179 <211> LENGTH: 512
180 <212> TYPE: PRT
181 <213> ORGANISM: B. licheniformis
183 <400> SEQUENCE: 2
184 Met Lys Gln Gln Lys Arg Leu Tyr Ala Arg Leu Leu Thr Leu Leu Phe
185 1 5 10 15
186 Ala Leu Ile Phe Leu Leu Pro His Ser Ala Ala Ala Ala Ala Asn Leu
187 20 25 30
188 Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro Asn Asp Gly
189 35 40 45
190 Gln His Trp Arg Arg Leu Gln Asn Asp Ser Ala Tyr Leu Ala Glu His
191 50 55 60
192 Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Thr Ser Gln
193 65 70 75 80
194 Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu Phe
195 85 90 95

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196 His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu Leu
197      100      105      110
198 Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn Val Tyr Gly
199      115      120      125
200 Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr Glu Asp Val
201      130      135      140
202 Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val Ile Ser Gly
203      145      150      155      160
204 Glu His Leu Ile Lys Ala Trp Thr His Phe His Phe Pro Gly Arg Gly
205      165      170      175
206 Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly Thr
207      180      185      190
208 Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys Phe Gln Gly
209      195      200      205
210 Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn Tyr Asp Tyr
211      210      215      220
212 Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val Ala Ala Glu
213      225      230      235      240
214 Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln Leu Asp Gly
215      245      250      255
216 Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe Leu Arg Asp
217      260      265      270
218 Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met Phe Thr Val
219      275      280      285
220 Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn Tyr Leu Asn
221      290      295      300
222 Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu His Tyr Gln
223      305      310      315      320
224 Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met Arg Lys Leu
225      325      330      335
226 Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ser Val Thr Phe
227      340      345      350
228 Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr Val
229      355      360      365
230 Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg Glu
231      370      375      380
232 Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys Gly
233      385      390      395      400
234 Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile Glu Pro Ile
235      405      410      415
236 Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His Asp Tyr Phe
237      420      425      430
238 Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser Val
239      435      440      445
240 Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly Ala
241      450      455      460
242 Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr Trp His Asp
243      465      470      475      480
244 Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser Glu Gly Trp

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245          485          490          495
246 Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr Val Gln Arg
247          500          505          510
249 <210> SEQ ID NO: 3
250 <211> LENGTH: 2084
251 <212> TYPE: DNA
252 <213> ORGANISM: B. amyloliquefaciens
254 <220> FEATURE:
255 <221> NAME/KEY: CDS
256 <222> LOCATION: (250)...(1791)
258 <221> NAME/KEY: mat_peptide
259 <222> LOCATION: (343)...(1791)
261 <221> NAME/KEY: sig_peptide
262 <222> LOCATION: (250)...(342)
264 <400> SEQUENCE: 3
265 gcccgcacac tacgaaaaga ctggctgaaa acattgagcc ttgatgact gatgatttgg      60
266 ctgaagaagt ggatcgattg tttagaaaaa gaagaagacc ataaaaatac cttgtctgtc      120
267 atcagacagg gtatttttta tgctgtccag actgtccgct gtgtaaaaat aaggaataaa      180
268 ggggggttgt tattatttta ctgatatgta aaatataatt tgtataagaa aatgagaggg      240
269 agaggaaac atg att caa aaa cga aag cgg aca gtt tcg ttc aga ctt gtg      291
270      Met Ile Gln Lys Arg Lys Arg Thr Val Ser Phe Arg Leu Val
271      -30      -25      -20
273 ctt atg tgc acg ctg tta ttt gtc agt ttg ccg att aca aaa aca tca      339
274 Leu Met Cys Thr Leu Leu Phe Val Ser Leu Pro Ile Thr Lys Thr Ser
275      -15      -10      -5
277 gcc gta aat ggc acg ctg atg cag tat ttt gaa tgg tat acg ccg aac      387
278 Ala Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn
279      1      5      10      15
281 gac ggc cag cat tgg aaa cga ttg cag aat gat gcg gaa cat tta tcg      435
282 Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser
283      20      25      30
285 gat atc gga atc act gcc gtc tgg att cct ccc gca tac aaa gga ttg      483
286 Asp Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu
287      35      40      45
289 agc caa tcc gat aac gga tac gga cct tat gat ttg tat gat tta gga      531
290 Ser Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly
291      50      55      60
293 gaa ttc cag caa aaa ggg acg gtc aga acg aaa tac ggc aca aaa tca      579
294 Glu Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser
295      65      70      75
297 gag ctt caa gat gcg atc gcc tca ctg cat tcc cgg aac gtc caa gta      627
298 Glu Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val
299      80      85      90      95
301 tac gga gat gtg gtt ttg aat cat aag gct ggt gct gat gca aca gaa      675
302 Tyr Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu
303      100      105      110
305 gat gta act gcc gtc gaa gtc aat ccg gcc aat aga aat cag gaa act      723
306 Asp Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr
307      115      120      125

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